

December 6, 2011

Contents

1	Summary	1
2	Dependencies	2
3	Description of Datasets	2
3.1	Brad's Phylo Stats	2
4	Import Data	3
5	Bray-Curtis Dissimilarity Based Partial-Correlations	4
6	Figures	6
7	Tables	10

1 Summary

- Question: Does phylogenetic history predict the effect of alpine cushion species on the interactions among associated species?
- Approach:
 1. Using a world-wide alpine plant database, generate covariance based models of interactions among other plant species.
 2. Identify
- Modeling:
 1. Partial correlations are generated using a distance based metric of correlation

2 Dependencies

3 Description of Datasets

3.1 Brad's Phylo Stats

- Number of paired plots
- Species richness
- Mean z-score of net relatedness index with all plots pooled (cushion and open). The z-score is based on comparison with an independent swap null model (see Picante R library > ses.mpd function for details, and Gotelli 2000 Ecology). NRI is $-1 \times \text{MPD}$, where MPD is mean pairwise (phylogenetic) distance among all species within a plot (see Swenson et al. 2006 Ecology)
- Standard error of above (sample size=2n)
- Mean z-score of NRI in cushions only. The species pool for the null model includes all species in the community, even if they do not occur in cushions.
- Standard error of above
- Mean z-score of NRI in open only.
- Standard error of above
- Mean pairwise distance separating taxa in paired cushion and open plots, a measure of phylobetadiversity. This can be compared to the phylobetadiversity across cushions and across open plots (see below) to estimate the relative phylogenetic turnover between versus within microhabitat types (i.e., there is no null model that this is compared to)
- Standard error of above
- MPD across cushions
- Standard error of above
- MPD across open plots. VALUE indicates insufficient number of species to calculate the index
- Standard error of above

- Other Data:

Test of phylogenetic signal in microhabitat preference, Blomberg's K; there is rarely enough statistical power for this test, due to the relatively small number of species, but when phylogenetic signal is significant it is one of divergence (i.e. close relatives have different microhabitat preferences); see `phylosignal` function in `picante`

Several phylogenetic diversity indices (see `Picante`)

4 Import Data

```
> if (load.data == TRUE) {
+   if (any(ls() == "mywd")) {
+     }
+   else {
+     mywd <- getwd()
+   }
+   setwd("data")
+   cush.data <- list()
+   for (i in 1:length(dir())) {
+     cush.data[[i]] <- read.csv(dir()[i])
+   }
+   names(cush.data) <- paste(lapply(cush.data, function(x) colnames(x)[2]),
+     dir(), sep = "_")
+   cush.site <- substr(dir(), 1, 7)
+   cush.site <- unlist(lapply(strsplit(cush.site, split = "\\."),
+     function(x) x[1])))
+   setwd(mywd)
+   as.character(unique(unlist(lapply(cush.data, function(x) x[,
+     4])))))
+   for (i in 1:length(cush.data)) {
+     cush.data[[i]][is.na(cush.data[[i]])] <- 0
+   }
+   cush.data <- lapply(cush.data, function(x) data.frame(x[,
+     1:4], rm.spp(x[, 5:ncol(x)], n = 10)))
+   cush.com <- lapply(cush.data, function(x) x[, 5:ncol(x)])
+   cush.com <- lapply(cush.com, na.omit)
+   cush.rep <- lapply(cush.data, function(x) x[, 3])
+ }
```

```

+     cush.micro <- lapply(cush.data, function(x) x[, 4])
+ } else {
+ }

```

5 Bray-Curtis Dissimilarity Based Partial-Correlations

```

> if (run.models == TRUE) {
+   cush.ind <- list()
+   along <- 1:length(cush.com)
+   for (i in along) {
+     x <- cush.com[[i]]
+     x.in <- x[cush.micro[[i]] == "cushion", ]
+     x.out <- x[cush.micro[[i]] == "open", ]
+     x.in <- x.in[, apply(x.in, 2, sum) != 0]
+     x.out <- x.out[, apply(x.out, 2, sum) != 0]
+     plot(hclust(vegdist(t(x.in))))
+     d <- as.matrix(vegdist(t(x.in)))
+     ind.in <- ind.net(d, nrow(x.in), alpha = 0.05, fix.na = TRUE,
+       fix.inf = TRUE)
+     d <- as.matrix(vegdist(t(x.out)))
+     ind.out <- ind.net(d, nrow(x.out), alpha = 0.05, fix.na = TRUE,
+       fix.inf = TRUE)
+     cush.ind[[i]] <- conform(ind.in, ind.out)
+     names(cush.ind[[i]]) <- c("cushion", "open")
+   }
+ } else {
+ }
> cush.n <- as.numeric(lapply(cush.micro, function(x) length(x[x ==
+   "open"])))
> ind.in <- lapply(cush.ind, function(x) x[[1]])
> ind.out <- lapply(cush.ind, function(x) x[[2]])
> deg.in <- as.numeric(lapply(ind.in, function(x) length(x[x !=
+   0])))
> deg.out <- as.numeric(lapply(ind.out, function(x) length(x[x !=
+   0])))
> cor(deg.in, cush.n)

```

```

[1] 0.5107984

```

```

> cor(deg.out, cush.n)

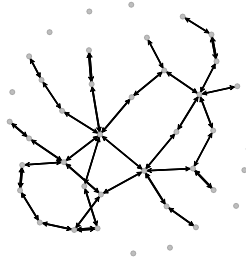
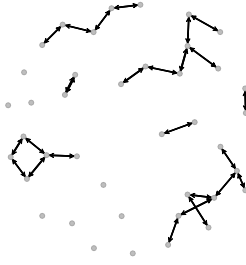
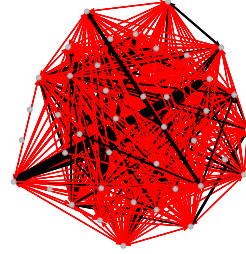
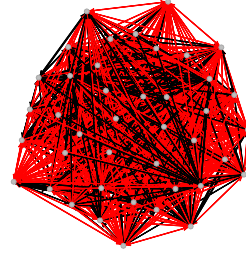
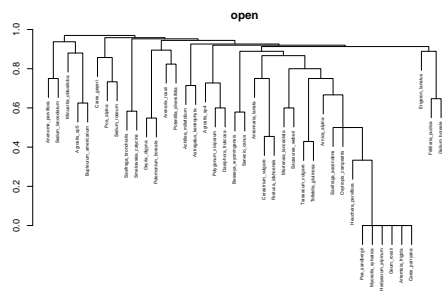
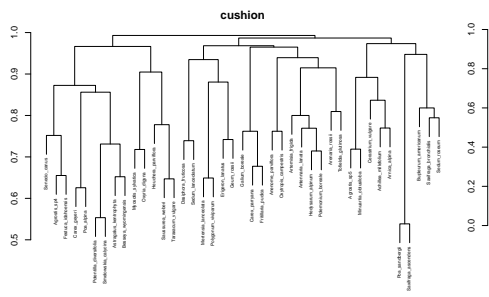
[1] 0.4004736

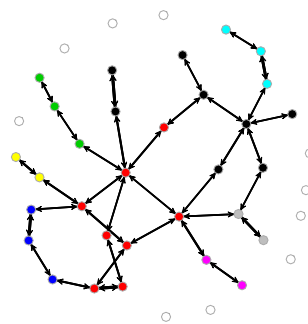
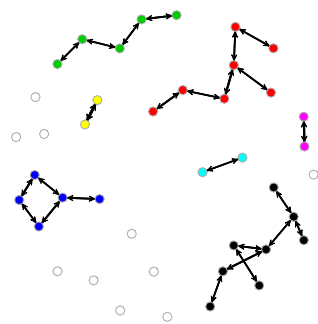
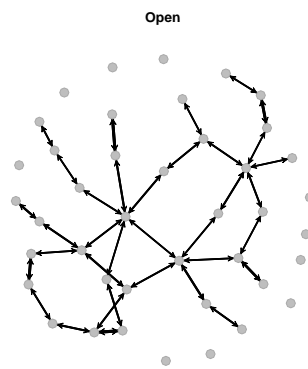
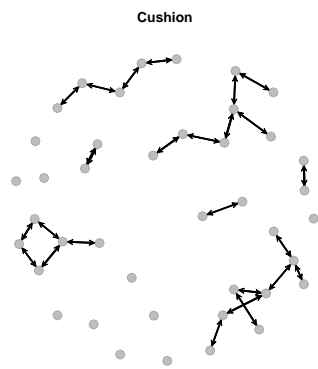
> plot(cush.n, deg.in, ylim = c(0, max(c(deg.in, deg.out))), pch = 19,
+      col = "black", ylab = "Number of Connections", xlab = "Number of Cushions Sam
> points(cush.n, deg.out, pch = 1, col = "black")
> abline(lm(deg.in ~ cush.n), lty = 2)
> abline(lm(deg.out ~ cush.n), lty = 1)
> legend("topleft", legend = c("Cushion", "Open"), pch = c(19,
+      1))
> phylo <- read.csv("/Users/Aeolus/Documents/Active_Projects/FacilitationNetworks/G
> phylo <- phylo[order(phylo$Sites), ]
> mod.in <- list()
> mod.in <- lapply(ind.in, function(x) getModules(x)[[2]])
> nmod.in <- unlist(lapply(mod.in, max))
> isol.in <- unlist(lapply(mod.in, function(x) length(x[x == 0])))
> mod.out <- list()
> mod.out <- lapply(ind.out, function(x) getModules(x)[[2]])
> nmod.out <- unlist(lapply(mod.out, max))
> isol.out <- unlist(lapply(mod.out, function(x) length(x[x ==
+      0])))
> m.in <- numeric()
> for (i in 1:length(mod.in)) {
+   x <- round(ind.in[[i]], 2)
+   y <- mod.in[[i]]
+   x <- x[y != 0, y != 0]
+   y <- y[y != 0]
+   x <- graph.adjacency(x, weighted = TRUE, mode = "undirected")
+   m.in[[i]] <- modularity(x, y)
+ }
> m.out <- numeric()
> for (i in 1:length(mod.out)) {
+   x <- round(ind.out[[i]], 2)
+   y <- mod.out[[i]]
+   x <- x[y != 0, y != 0]
+   y <- y[y != 0]
+   x <- graph.adjacency(x, weighted = TRUE, mode = "undirected")
+   m.out[[i]] <- modularity(x, y)

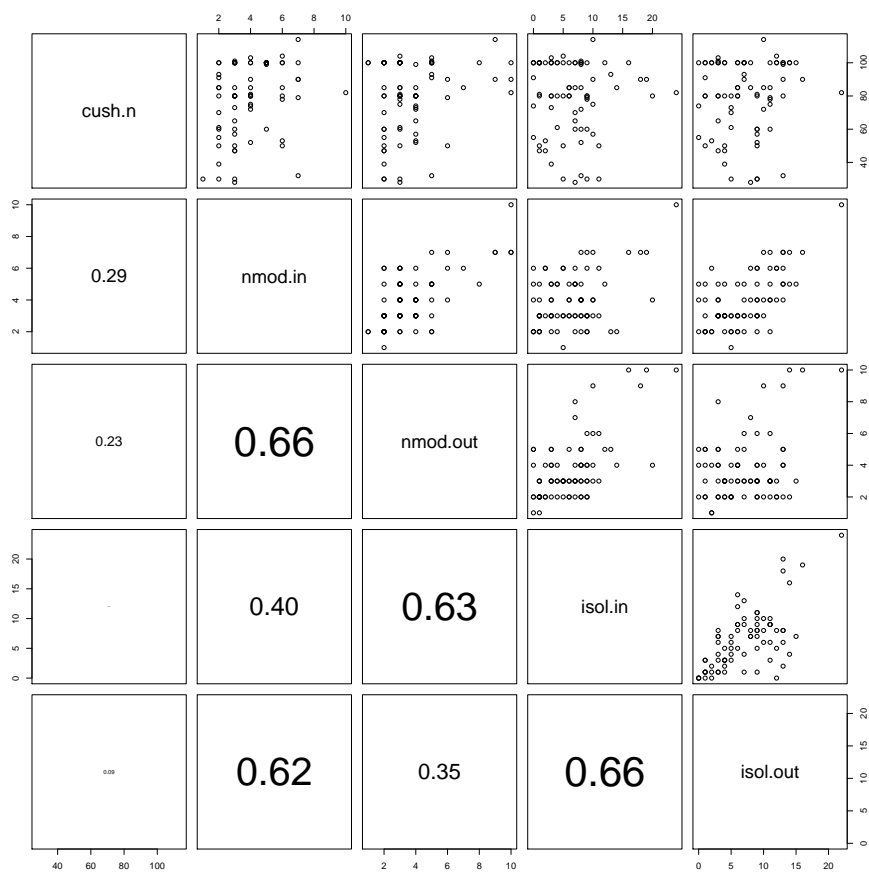
```

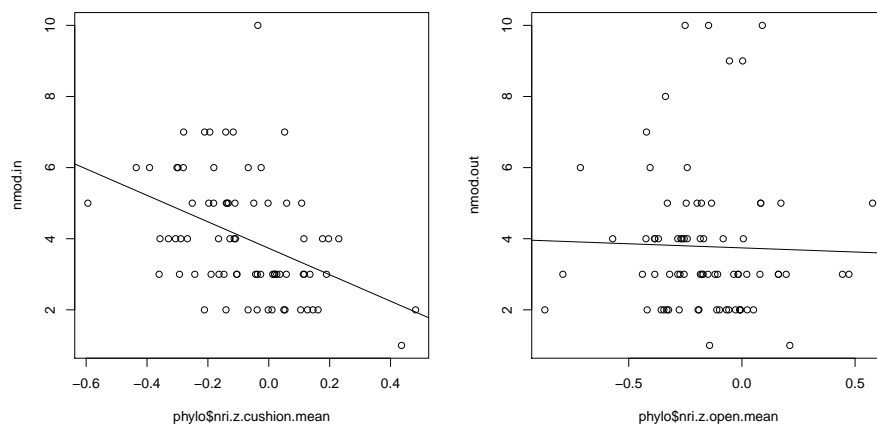
```
+ }  
> m.in[is.na(m.in)] <- 0  
> m.out[is.na(m.out)] <- 0  
> all(as.character(phylo$Sites) == cush.site)  
  
[1] TRUE
```

6 Figures









7 Tables

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.7320	0.1924	19.40	0.0000
NRI.z.cushion	-3.7202	0.9456	-3.93	0.0002

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.7423	0.2784	13.44	0.0000
NRI.z.open	-0.2317	0.9432	-0.25	0.8066